DOCKET NO.: DIBIS-0003US (Counsel Docket No. 10310) **PATENT**

IN THE CLAIMS:

1-68. (previously cancelled)

69. (currently amended) A method for providing ~~bacterial~~ bioagent characterizing information comprising:

a) measuring or calculating with a mass spectrometer a plurality of molecular masses corresponding to a plurality of amplification products, wherein the amplification products are 46 to 166 nucleobases in length, and wherein the amplification products are obtained by amplification of at least one target sequence region of a ~~a segment of bacterial~~ bioagent nucleic acid gene sequence ~~with a~~ using a primer pair that hybridizes to ~~nucleic acid of about one hundred or more bacterial~~ the at least one target sequence region of at least eight bioagents ~~at conserved regions that flank an intervening variable region~~; said target sequence region comprising two conserved regions that are hybridizable with the primer pair and that flank a variable region that varies between at least eight bioagents;

b) interrogating a database stored on a computer readable medium with an identification query, wherein the identification query comprises comparison of the [[a]] measured molecular mass of step a) with the database; ~~an amplification product 46 to 166 nucleobases in length of nucleic acid of a bacterial bioagent obtained upon amplification with the primer pair, and wherein the~~ said database comprises molecular mass calculated for the target sequence regions for at least eight bioagents and each of the ~~some members of the measured or calculated plurality of molecular masses of step a) wherein each member of the plurality of measured or~~ calculated molecular masses is indexed to ~~bacterial~~ bioagent characterizing information;

c) delivering from the database a response that comprises the ~~bacterial~~ bioagent characterization information generated by the comparison of the measured and calculated molecular mass of step b) thereby identifying the bioagent associated with amplification product of step a) ~~with the measured or calculated molecular masses of step a) contained in the database~~.

70. (currently amended) The method of claim 69 wherein the nucleic acid gene sequence encodes ribosomal RNA or a protein involved in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, energy generation, uptake, or secretion.

71. (previously presented) The method of claim 69 wherein the bioagent characterizing information is a genus name.

72. (previously presented) The method of claim 71 wherein the genus name is *Acinetobacter*, *Aeromonas*, *Bacillus*, *Bacteriodes*, *Bartonella*, *Bordetella*, *Borrelia*, *Brucella*, *Burkholderia*, *Campylobacter*, *Chlamydia*, *Chlamydophila*, *Clostridium*, *Coxiella*, *Enterococcus*, *Escherichia*, *Francisella*, *Fusobacterium*, *Haemophilus*, *Helicobacter*, *Klebsiella*, *Legionella*, *Leptospira*, *Listeria*, *Moraxella*, *Mycobacterium*, *Mycoplasma*, *Neisseria*, *Proteus*, *Pseudomonas*, *Rhodobacter*, *Rickettsia*, *Salmonella*, *Shigella*, *Staphylococcus*, *Streptobacillus*, *Streptomyces*, *Treponema*, *Ureaplasma*, *Vibrio*, or *Yersinia*.

73. (previously presented) The method of claim 69 wherein the bioagent characterizing information is a species name.

74. (previously presented) The method of claim 69 wherein the bioagent characterizing information is a strain name.

75. (previously presented) The method of claim 69 wherein the response is delivered via a network.

76. (previously presented) The method of claim 75 wherein the network is a local area network, a wide area network, or the internet.

77. (canceled)

78. (currently amended) The method of claim ~~77~~ 69 wherein ~~the~~ said mass ~~spectrometry~~ spectrometer is an electrospray Fourier transform ion cyclotron resonance mass ~~spectrometry~~ spectrometer or an electrospray time-of-flight mass ~~spectrometry~~ spectrometer.

79. (currently amended) The method of claim 69 wherein ~~the~~ said eight or more amplification products comprise a variable region between primer hybridization sites ~~has~~ having no greater than 5% sequence identity among the ~~one hundred~~ eight or more ~~bacterial~~ bioagents.

80. (previously presented) The method of claim 69 wherein the primer pair comprises at least one modified nucleobase.

81. (previously presented) The method of claim 80 wherein the modified nucleobase comprises 2,6-diaminopurine, propyne C, propyne T, phenoxazine, or G-clamp.

82. (currently amended) The method of claim 69 wherein ~~the bacterial~~ said bioagent is a biological warfare agent.

83. (previously presented) The method of claim 82 wherein the biological warfare agent comprises *Bacillus anthracis, Yersinia pestis, Franciscella tularensis, Brucella suis, Brucella abortus, Brucella melitensis, Burkholderia mallei, Burkholderia pseudomalleii, Salmonella typhi, Rickettsia typhii, Rickettsia prowasekii, Coxiella burnetii, Rhodobacter capsulatus, Chlamydia pneumoniae, Escherichia coli, Shigella dysenteriae, Shigella flexneri, Bacillus cereus, Clostridium botulinum, Coxiella burnetti, Pseudomonas aeruginosa, Legionella pneumophila, or Vibrio cholerae.*

84. (currently amended) The method of claim 69 wherein the ~~conserved regions~~ primer hybridization sites of said amplification products have between 80-100% sequence identity among ~~the one hundred~~ said eight or more ~~bacterial~~ bioagents.

85. (currently amended) A method for providing ~~bacterial~~ bioagent characterizing information comprising:

a) measuring or calculating with a mass spectrometer a plurality of molecular masses ~~base compositions~~ corresponding to a plurality of amplification products, wherein the amplification products are 46 to 166 nucleobases in length, and wherein the amplification products are obtained by amplification of at least one target sequence of a ~~a segment of bacterial~~ bioagent nucleic acid gene sequence ~~with a~~ using a primer pair that hybridizes to the at least one target sequence region of at least eight bioagents ~~nucleic acid of about one hundred or more bacterial bioagents at conserved regions that flank an intervening variable region~~ said target sequence region comprising two conserved regions that are hybridizable with the primer pair and that flank a variable region that varies between at least eight bioagents;

b) calculating a base composition from said molecular mass measurement, wherein it identifies the number of A residues, C residues, T residues, G residues, U residues, analogues thereof and mass tag residues thereof;

~~b)~~ c) interrogating a database stored on a computer readable medium with an identification query, wherein the identification query comprises comparison of the base composition data from step b) with the database; said ~~a measured base composition of an amplification product 46 to 166 nucleobases in length of nucleic acid of a bacterial bioagent obtained upon amplification with the primer pair, and wherein the~~ database comprises base composition data calculated for the target sequence regions for at least eight of the bioagents and each of the ~~at least some members of the measured or calculated plurality of base compositions of step a) wherein each member of the plurality of measured or~~ calculated base compositions is indexed to ~~bacterial~~ bioagent characterizing information; and

~~c)~~ d) delivering from the database a response ~~to said step of interrogating said database wherein said response comprises bacterial~~ comprising bioagent characterization information generated by the comparison of said measured and calculated base composition of step c) thereby identifying the bioagent associated with an amplification product of step a) ~~molecular mass of step b) with said measured or calculated base compositions of step a) contained in said database~~.

86. (currently amended) The method of claim 85 wherein the nucleic acid gene sequence encodes ribosomal RNA or a protein involved in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, energy generation, uptake, or secretion.

87. (previously presented) The method of claim 85 wherein the bioagent characterizing information is a genus name.

88. (previously presented) The method of claim 87 wherein the genus name is *Acinetobacter*, *Aeromonas*, *Bacillus*, *Bacteriodes*, *Bartonella*, *Bordetella*, *Borrelia*, *Brucella*, *Burkholderia*, *Campylobacter*, *Chlamydia*, *Chlamydophila*, *Clostridium*, *Coxiella*, *Enterococcus*, *Escherichia*, *Francisella*, *Fusobacterium*, *Haemophilus*, *Helicobacter*, *Klebsiella*, *Legionella*, *Leptospira*, *Listeria*, *Moraxella*, *Mycobacterium*, *Mycoplasma*, *Neisseria*, *Proteus*, *Pseudomonas*, *Rhodobacter*, *Rickettsia*, *Salmonella*, *Shigella*, *Staphylococcus*, *Streptobacillus*, *Streptomyces*, *Treponema*, *Ureaplasma*, *Vibrio*, or *Yersinia*.

89. (previously presented) The method of claim 85 wherein the bioagent characterizing information is a species name.

90. (previously presented) The method of claim 85 wherein the bioagent characterizing information is a strain name.

91. (previously presented) The method of claim 85 wherein the response is delivered via a network.

92. (previously presented) The method of claim 91 wherein the network is a local area network, a wide area network, or the internet.

93. (canceled)

94. (currently amended) The method of claim ~~93~~ 85 wherein ~~the~~ said mass ~~spectrometry~~ spectrometer is an electrospray Fourier transform ion cyclotron resonance mass spectrometer or an electrospray time-of-flight mass spectrometer.

95. (currently amended) The method of claim 85 wherein ~~the~~ said eight or more amplification products comprise a variable region between primer hybridization sites ~~has~~ having no greater than 5% sequence identity among the ~~one hundred~~ eight or more ~~bacterial~~ bioagents.

96. (previously presented) The method of claim 85 wherein the primer pair comprises at least one modified nucleobase.

97. (previously presented) The method of claim 96 wherein the modified nucleobase comprises 2,6-diaminopurine, propyne C, propyne T, phenoxazine, or G-clamp.

98. (currently amended) The method of claim 85 wherein ~~the bacterial~~ said bioagent is a biological warfare agent.

99. (previously presented) The method of claim 98 wherein the biological warfare agent comprises *Bacillus anthracis, Yersinia pestis, Franciscella tularensis, Brucella suis, Brucella abortus, Brucella melitensis, Burkholderia mallei, Burkholderia pseudomalleii, Salmonella typhi, Rickettsia typhii, Rickettsia prowasekii, Coxiella burnetii, Rhodobacter capsulatus, Chlamydia pneumoniae, Escherichia coli, Shigella dysenteriae, Shigella flexneri, Bacillus cereus, Clostridium botulinum, Coxiella burnetti, Pseudomonas aeruginosa, Legionella pneumophila, or Vibrio cholerae.*

100. (currently amended) The method of claim 85 wherein ~~the conserved regions~~ primer hybridization sites of said amplification products have between 80-100% sequence identity among ~~the one hundred~~ said eight or more ~~bacterial~~ bioagents.

101. (new) The method of claim 69 wherein said bioagent is a bacterium, virus, fungus or protozoan.

102. (new) The method of claim 101 wherein the bioagent is arenavirus, bunyavirus, mononegavirales, picornavirus, astrovirus, calcivirus, nidovirales, flavivirus or togavirus.

103. (new) The method of claim 85 wherein said bioagent is a bacterium, virus, fungus or protozoan.

104. (new) The method of claim 103 wherein the bioagent is arenavirus, bunyavirus, mononegavirales, picornavirus, astrovirus, calcivirus, nidovirales, flavivirus or togavirus.